



SEQUENCE LISTING

<110> BLEDSOE, RANDY K
LAMBERT, MILLARD H
MONTANA, VALERIE G
STEWART, EUGENE L
XU, H. ERIC

<120> METHOD FOR IDENTIFYING A GLUCOCORTICOID
RECEPTOR MODULATOR USING THE STRUCTURE OF A GLUCOCORTICOID
RECEPTOR LIGAND BINDING DOMAIN (TITLE AS AMENDED)

<130> PU4803 US

<140> US 10/600,751

<141> 2003-06-20

<150> US 60/390,610

<151> 2002-06-21

<160> 14

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<212> DNA

<213> Homo Sapiens

<220>

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Asp Gln Cys Lys His Met Leu Tyr Val Ser Ser Glu Leu His Arg Leu	
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Ile Arg Met Thr Tyr Ile Lys Glu Leu Gly Lys Ala Ile Val Lys Arg	
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Glu Gly Asn Ser Ser Gln Asn Trp Gln Arg Phe Tyr Gln Leu Thr Lys	
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ctc ttg gat tct atg cat gaa gtg gtt gaa aat ctc ctt aac tat tgc	2208
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Phe Gln Thr Phe Leu Asp Lys Thr Met Ser Ile Glu Phe Pro Glu Met	
740 745 750	
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Phe Pro Lys Gly Ser Val Ser Asn Ala Gln Gln Pro Asp Leu Ser Lys	
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Ala Val Ser Leu Ser Met Gly Leu Tyr Met Gly Glu Thr Glu Thr Lys	
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Val Met Gly Asn Asp Leu Gly Phe Pro Gln Gln Gly Gln Ile Ser Leu	
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Leu Asn Arg Ser Thr Ser Val Pro Glu Asn Pro Lys Ser Ser Ala Ser	

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Ser Asp Val Ser Ser	Glu Gln Gln His Leu Lys	Gly Gln Thr Gly Thr
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Asn Gly Gly Asn Val	Lys Leu Tyr Thr Thr	Asp Gln Ser Thr Phe Asp
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Ile Leu Gln Asp Leu	Glu Phe Ser Ser Gly Ser	Pro Gly Lys Glu Thr
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Asn Glu Ser Pro Trp	Arg Ser Asp Leu Leu Ile	Asp Glu Asn Cys Leu
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Leu Ser Pro Leu Ala	Gly Glu Asp Asp Ser Phe	Leu Leu Glu Gly Asn
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Ser Asn Glu Asp Cys	Lys Pro Leu Ile Leu Pro	Asp Thr Lys Pro Lys
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Val His Gly Val Ser	Thr Ser Gly Gly Gln Met	Tyr His Tyr Asp Met
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Val Ile Pro Pro Ile	Pro Val Gly Ser Glu Asn	Trp Asn Arg Cys Gln
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Gly Arg Thr Val Phe	Ser Asn Gly Tyr Ser Ser	Pro Ser Met Arg Pro
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Pro Pro Lys Leu Cys	Leu Val Cys Ser Asp	Glu Ala Ser Gly Cys His
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Tyr Gly Val Leu Thr	Cys Gly Ser Cys Lys Val	Phe Phe Lys Arg Ala
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Val Glu Gly Gln His	Asn Tyr Leu Cys Ala Gly	Arg Asn Asp Cys Ile
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Ile Asp Lys Ile Arg	Arg Lys Asn Cys Pro Ala	Cys Arg Tyr Arg Lys
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Cys Leu Gln Ala Gly	Met Asn Leu Glu Ala Arg	Lys Thr Lys Lys Lys
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Ile Lys Gly Ile Gln	Gln Ala Thr Thr Gly Val	Ser Gln Glu Thr Ser
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Glu Asn Pro Gly Asn	Lys Thr Ile Val Pro Ala	Thr Leu Pro Gln Leu
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Thr Pro Thr Leu Val	Ser Leu Leu Glu Val Ile	Glu Pro Glu Val Leu
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Tyr Ala Gly Tyr Asp	Ser Ser Val Pro Asp Ser	Thr Trp Arg Ile Met
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Thr Thr Leu Asn Met	Leu Gly Gly Arg Gln Val	Ile Ala Ala Val Lys
	565	570
Trp Ala Lys Ala Ile	Pro Gly Phe Arg Asn Leu	His Leu Asp Asp Gln
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Met Thr Leu Leu Gln	Tyr Ser Trp Met Phe Leu	Met Ala Phe Ala Leu
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Gly Trp Arg Ser Tyr	Arg Gln Ser Ser Ala Asn	Leu Leu Cys Phe Ala
	610	615
Pro Asp Leu Ile Ile	Asn Glu Gln Arg Met Thr	Leu Pro Cys Met Tyr
625	630	635
Asp Gln Cys Lys His	Met Leu Tyr Val Ser Ser	Glu Leu His Arg Leu

Gln	Val	Ser	Tyr	645	Glu	Glu	Tyr	Leu	Cys	650	Met	Lys	Thr	Leu	Leu	655	Leu	Leu
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Ile	Arg	Met	Thr	675	Tyr	Ile	Lys	Glu	Leu	680	Gly	Lys	Ala	Ile	Val	685	Lys	Arg
Glu	Gly	Asn	Ser	690	Ser	Gln	Asn	Trp	Gln	695	Arg	Phe	Tyr	Gln	Leu	700	Thr	Lys
Leu	Leu	Asp	Ser	705	Met	His	Glu	Val	Val	710	Glu	Asn	Leu	Leu	Asn	715	Tyr	Cys
Phe	Gln	Thr	Phe	720	Leu	Asp	Lys	Thr	Met	725	Ser	Ile	Glu	Phe	Pro	730	Glu	Met
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gtg	atg	gga	aat	gac	ctg	gga	ttc	cca	cag	cag	ggc	caa	atc	agc	ctt		336
Val	Met	Gly	Asn	Asp	Leu	Gly	Phe	Pro	Gln	Gln	Gly	Gln	Ile	Ser	Leu		
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Leu	Asn	Arg	Ser	Thr	Ser	Val	Pro	Glu	Asn	Pro	Lys	Ser	Ser	Ala	Ser		
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Asn	Thr	Ala	Ser	Leu	Ser	Gln	Gln	Gln	Asp	Gln	Lys	Pro	Ile	Phe	Asn	
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Val	Ile	Pro	Pro	Ile	Pro	Val	Gly	Ser	Glu	Asn	Trp	Asn	Arg	Cys	Gln	
		355				360						365				
gga	tct	gga	gat	gac	aac	ttg	act	tct	ctg	ggg	act	ctg	aac	ttc	cct	1152
Gly	Ser	Gly	Asp	Asp	Asn	Leu	Thr	Ser	Leu	Gly	Thr	Leu	Asn	Phe	Pro	
		370				375					380					
ggt	cga	aca	gtt	ttt	tct	aat	ggc	tat	tca	agc	ccc	agc	atg	aga	cca	1200
Gly	Arg	Thr	Val	Phe	Ser	Asn	Gly	Tyr	Ser	Ser	Pro	Ser	Met	Arg	Pro	
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gat gta agc tct cct cca tcc agc tcc tca aca gca aca aca gga cca	1248
Asp Val Ser Ser Pro 405 Ser Ser Ser Thr Ala Thr Thr Gly Pro 415	
cct ccc aaa ctg tgc ctg gtg tgc tct gat gaa gct tca gga tgt cat	1296
Pro Pro Lys Leu Cys Leu Val Cys Ser Asp Glu Ala Ser Gly Cys His 420 425 430	
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Tyr Gly Val Leu Thr Cys Gly Ser Cys Lys Val Phe Phe Lys Arg Ala 435 440 445	
gtg gaa gga cag cac aat tac cta tgt gct gga agg aat gat tgc atc	1392
Val Glu Gly Gln His Asn Tyr 455 Leu Cys Ala Gly Arg Asn Asp Cys Ile 450 460	
atc gat aaa att cga aga aaa aac tgc cca gca tgc cgc tat cga aaa	1440
Ile Asp Lys Ile Arg Arg Lys Asn Cys Pro Ala Cys Arg Tyr Arg Lys 465 470 475 480	
tgt ctt cag gct gga atg aac ctg gaa gct cga aaa aca aag aaa aaa	1488
Cys Leu Gln Ala Gly Met Asn Leu Glu Ala Arg Lys Thr Lys Lys Lys 485 490 495	
ata aaa gga att cag cag gcc act aca gga gtc tca caa gaa acc tct	1536
Ile Lys Gly Ile Gln Gln Ala Thr 505 Gly Val Ser Gln Glu Thr Ser 500 510	
gaa aat cct ggt aac aaa aca ata gtt cct gca acg tta cca caa ctg	1584
Glu Asn Pro Gly Asn Lys Thr 520 Val Pro Ala Thr Leu Pro Gln Leu 515 525	
acc cct acc ctg gtg tca ctg ttg gag gtt att gaa cct gaa gtg tta	1632
Thr Pro Thr Leu Val Ser Leu Leu Glu Val Ile Glu Pro Glu Val Leu 530 535 540	
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Tyr Ala Gly Tyr Asp Ser Ser Val Pro Asp Ser Thr Trp Arg Ile Met 545 550 555 560	
act acg ctg aac atg tta gga ggg cgg caa gtg att gca gca gtg aaa	1728
Thr Thr Leu Asn Met Leu Gly Gly Arg Gln Val Ile Ala Ala Val Lys 565 570 575	
tgg gca aag gca ata cca ggt ttc agg aac tta cac ctg gat gac caa	1776
Trp Ala Lys Ala Ile Pro Gly Phe Arg Asn Leu His Leu Asp Asp Gln 580 585 590	
atg acc cta ctg cag tac tcc tgg atg tcc ctt atg gca ttt gct ctg	1824
Met Thr Leu Leu Gln Tyr Ser Trp 600 Met Ser Leu Met Ala Phe Ala Leu 595 605	
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Gly Trp Arg Ser Tyr Arg Gln Ser Ser Ala Asn Leu Leu Cys Phe Ala 610 615 620	
cct gat ctg att att aat gag cag aga atg act cta ccc tgc atg tac	1920
Pro Asp Leu Ile Ile Asn Glu Gln Arg Met Thr Leu Pro Cys Met Tyr 625 630 635 640	
gac caa tgt aaa cac atg ctg tat gtt tcc tct gag tta cac agg ctt	1968
Asp Gln Cys Lys His 645 Met Leu Tyr Val Ser Ser Glu Leu His Arg Leu 650 655	

cag gta tct tat gaa gag tat ctc tgt atg aaa acc tta ctg ctt ctc	2016
Gln Val Ser Tyr 660 Glu Glu Tyr Leu Cys Met Lys Thr Leu Leu Leu Leu 670	
tct tca gtt cct aag gac ggt ctg aag agc caa gag cta ttt gat gaa	2064
Ser Ser Val Pro Lys Asp Gly Leu Lys Ser Gln Glu Leu Phe Asp Glu 675 680 685	
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Ile Arg Met Thr Tyr Ile Lys Glu Leu Gly Lys Ala Ile Val Lys Arg 690 695 700	
gaa gga aac tcc agc cag aac tgg cag cgg ttt tat caa ctg aca aaa	2160
Glu Gly Asn Ser Ser Gln Asn Trp Gln Arg Phe Tyr Gln Leu Thr Lys 705 710 715 720	
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Leu Leu Asp Ser Met His Glu Val Val Glu Asn Leu Leu Asn Tyr Cys 725 730 735	
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Phe Gln Thr Phe Leu Asp Lys Thr Met Ser Ile Glu Phe Pro Glu Met 740 745 750	
tta gct gaa atc atc acc aat cag ata cca aaa tat tca aat gga aat	2304
Leu Ala Glu Ile Ile Thr Asn Gln Ile Pro Lys Tyr Ser Asn Gly Asn 755 760 765	
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35 40 45
Ala Val Ala Ser Gln Ser Asp Ser Lys Gln Arg Arg Leu Leu Val Asp
50 55 60
Phe Pro Lys Gly Ser Val Ser Asn Ala Gln Gln Pro Asp Leu Ser Lys
65 70 75 80
Ala Val Ser Leu Ser Met Gly Leu Tyr Met Gly Glu Thr Glu Thr Lys
85 90 95
Val Met Gly Asn Asp Leu Gly Phe Pro Gln Gln Gly Gln Ile Ser Leu
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Ser Ser Gly Glu Thr Asp Leu Lys Leu Leu Glu Glu Ser Ile Ala Asn
115 120 125
Leu Asn Arg Ser Thr Ser Val Pro Glu Asn Pro Lys Ser Ser Ala Ser
130 135 140
Thr Ala Val Ser Ala Ala Pro Thr Glu Lys Glu Phe Pro Lys Thr His
145 150 155 160
Ser Asp Val Ser Ser Glu Gln Gln His Leu Lys Gly Gln Thr Gly Thr
165 170 175
Asn Gly Gly Asn Val Lys Leu Tyr Thr Asp Gln Ser Thr Phe Asp
180 185 190

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Ser	Asn	Glu	Asp	Cys	Lys	Pro	Leu	Ile	Leu	Pro	Asp	Thr	Lys	Pro	Lys
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Ile	Lys	Asp	Asn	Gly	Asp	Leu	Val	Leu	Ser	Ser	Pro	Ser	Asn	Val	Thr
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Leu	Pro	Gln	Val	Lys	Thr	Glu	Lys	Glu	Asp	Phe	Ile	Glu	Leu	Cys	Thr
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Pro	Gly	Val	Ile	Lys	Gln	Glu	Lys	Leu	Gly	Thr	Val	Tyr	Cys	Gln	Ala
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Ser	Phe	Pro	Gly	Ala	Asn	Ile	Ile	Gly	Asn	Lys	Met	Ser	Ala	Ile	Ser
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Val	His	Gly	Val	Ser	Thr	Ser	Gly	Gly	Gln	Met	Tyr	His	Tyr	Asp	Met
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Asn	Thr	Ala	Ser	Leu	Ser	Gln	Gln	Gln	Asp	Gln	Lys	Pro	Ile	Phe	Asn
			340					345					350		
Val	Ile	Pro	Pro	Ile	Pro	Val	Gly	Ser	Glu	Asn	Trp	Asn	Arg	Cys	Gln
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Pro	Pro	Lys	Leu	Cys	Leu	Val	Cys	Ser	Asp	Glu	Ala	Ser	Gly	Cys	His
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Tyr	Gly	Val	Leu	Thr	Cys	Gly	Ser	Cys	Lys	Val	Phe	Phe	Lys	Arg	Ala
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	450					455					460				
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Cys	Leu	Gln	Ala	Gly	Met	Asn	Leu	Glu	Ala	Arg	Lys	Thr	Lys	Lys	Lys
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			500					505					510		
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		515					520					525			
Thr	Pro	Thr	Leu	Val	Ser	Leu	Leu	Glu	Val	Ile	Glu	Pro	Glu	Val	Leu
	530					535					540				
Tyr	Ala	Gly	Tyr	Asp	Ser	Ser	Val	Pro	Asp	Ser	Thr	Trp	Arg	Ile	Met
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Thr	Thr	Leu	Asn	Met	Leu	Gly	Gly	Arg	Gln	Val	Ile	Ala	Ala	Val	Lys
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Trp	Ala	Lys	Ala	Ile	Pro	Gly	Phe	Arg	Asn	Leu	His	Leu	Asp	Asp	Gln
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Met	Thr	Leu	Leu	Gln	Tyr	Ser	Trp	Met	Ser	Leu	Met	Ala	Phe	Ala	Leu
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Gly	Trp	Arg	Ser	Tyr	Arg	Gln	Ser	Ser	Ala	Asn	Leu	Leu	Cys	Phe	Ala
	610					615					620				
Pro	Asp	Leu	Ile	Ile	Asn	Glu	Gln	Arg	Met	Thr	Leu	Pro	Cys	Met	Tyr
625					630					635					640
Asp	Gln	Cys	Lys	His	Met	Leu	Tyr	Val	Ser	Ser	Glu	Leu	His	Arg	Leu
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Gln	Val	Ser	Tyr	Glu	Glu	Tyr	Leu	Cys	Met	Lys	Thr	Leu	Leu	Leu	Leu
			660					665					670		
Ser	Ser	Val	Pro	Lys	Asp	Gly	Leu	Lys	Ser	Gln	Glu	Leu	Phe	Asp	Glu
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Ile	Arg	Met	Thr	Tyr	Ile	Lys	Glu	Leu	Gly	Lys	Ala	Ile	Val	Lys	Arg
	690					695					700				

Glu	Gly	Asn	Ser	Ser	Gln	Asn	Trp	Gln	Arg	Phe	Tyr	Gln	Leu	Thr	Lys
705					710					715					720
Leu	Leu	Asp	Ser	Met	His	Glu	Val	Val	Glu	Asn	Leu	Leu	Asn	Tyr	Cys
				725					730					735	
Phe	Gln	Thr	Phe	Leu	Asp	Lys	Thr	Met	Ser	Ile	Glu	Phe	Pro	Glu	Met
			740					745					750		
Leu	Ala	Glu	Ile	Ile	Thr	Asn	Gln	Ile	Pro	Lys	Tyr	Ser	Asn	Gly	Asn
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Glu	Val	Ile	Glu	Pro	Glu	Val	Leu	Tyr	Ala	Gly	Tyr	Asp	Ser	Ser	Val	
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cca gac tca act tgg agg atc atg act acg ctc aac atg tta gga ggg															144	
Pro	Asp	Ser	Thr	Trp	Arg	Ile	Met	Thr	Thr	Leu	Asn	Met	Leu	Gly	Gly	
			35				40					45				
cgg caa gtg att gca gca gtg aaa tgg gca aag gca ata cca ggt ttc															192	
Arg	Gln	Val	Ile	Ala	Ala	Val	Lys	Trp	Ala	Lys	Ala	Ile	Pro	Gly	Phe	
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agg aac tta cac ctg gat gac caa atg acc cta ctg cag tac tcc tgg															240	
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atg ttt ctt atg gca ttt gct ctg ggg tgg aga tca tat aga caa tca															288	
Met	Phe	Leu	Met	Ala	Phe	Ala	Leu	Gly	Trp	Arg	Ser	Tyr	Arg	Gln	Ser	
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agt gca aac ctg ctg tgt ttt gct cct gat ctg att att aat gag cag															336	
Ser	Ala	Asn	Leu	Leu	Cys	Phe	Ala	Pro	Asp	Leu	Ile	Ile	Asn	Glu	Gln	
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aga atg act cta ccc tgc atg tac gac caa tgt aaa cac atg ctg tat															384	
Arg	Met	Thr	Leu	Pro	Cys	Met	Tyr	Asp	Gln	Cys	Lys	His	Met	Leu	Tyr	
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ggt tcc tct gag tta cac agg ctt cag gta tct tat gaa gag tat ctc															432	
Val	Ser	Ser	Glu	Leu	His	Arg	Leu	Gln	Val	Ser	Tyr	Glu	Glu	Tyr	Leu	
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tgt atg aaa acc tta ctg ctt ctc tct tca gtt cct aag gac ggt ctg															480	
Cys	Met	Lys	Thr	Leu	Leu	Leu	Leu	Ser	Ser	Val	Pro	Lys	Asp	Gly	Leu	
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aag agc caa gag cta ttt gat gaa att aga atg acc tac atc aaa gag															528	
Lys	Ser	Gln	Glu	Leu	Phe	Asp	Glu	Ile	Arg	Met	Thr	Tyr	Ile	Lys	Glu	

165										170					175					
cta	gga	aaa	gcc	att	gtc	aag	agg	gaa	gga	aac	tcc	agc	cag	aac	tg	576				
Leu	Gly	Lys	Ala	Ile	Val	Lys	Arg	Glu	Gly	Asn	Ser	Ser	Gln	Asn	Trp					
			180					185					190							
cag	cgg	ttt	tat	caa	ctg	aca	aaa	ctc	ttg	gat	tct	atg	cat	gaa	gtg	624				
Gln	Arg	Phe	Tyr	Gln	Leu	Thr	Lys	Leu	Leu	Asp	Ser	Met	His	Glu	Val					
		195					200					205								
gtt	gaa	aat	ctc	ctt	aac	tat	tgc	ttc	caa	aca	ttt	ttg	gat	aag	acc	672				
Val	Glu	Asn	Leu	Leu	Asn	Tyr	Cys	Phe	Gln	Thr	Phe	Leu	Asp	Lys	Thr					
	210					215					220									
atg	agt	att	gaa	ttc	ccc	gag	atg	tta	gct	gaa	atc	atc	acc	aat	cag	720				
Met	Ser	Ile	Glu	Phe	Pro	Glu	Met	Leu	Ala	Glu	Ile	Ile	Thr	Asn	Gln					
225					230					235					240					
ata	cca	aaa	tat	tca	aat	gga	aat	atc	aaa	aaa	ctt	ctg	ttt	cat	caa	768				
Ile	Pro	Lys	Tyr	Ser	Asn	Gly	Asn	Ile	Lys	Lys	Leu	Leu	Phe	His	Gln					
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Lys	*																			

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Arg	Gln	Val	Ile	Ala	Ala	Val	Lys	Trp	Ala	Lys	Ala	Ile	Pro	Gly	Phe
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Ser	Ala	Asn	Leu	Leu	Cys	Phe	Ala	Pro	Asp	Leu	Ile	Ile	Asn	Glu	Gln
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Val	Ser	Ser	Glu	Leu	His	Arg	Leu	Gln	Val	Ser	Tyr	Glu	Glu	Tyr	Leu
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Cys	Met	Lys	Thr	Leu	Leu	Leu	Leu	Ser	Ser	Val	Pro	Lys	Asp	Gly	Leu
145					150					155					160
Lys	Ser	Gln	Glu	Leu	Phe	Asp	Glu	Ile	Arg	Met	Thr	Tyr	Ile	Lys	Glu
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Leu	Gly	Lys	Ala	Ile	Val	Lys	Arg	Glu	Gly	Asn	Ser	Ser	Gln	Asn	Trp
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Gln	Arg	Phe	Tyr	Gln	Leu	Thr	Lys	Leu	Leu	Asp	Ser	Met	His	Glu	Val
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Val	Glu	Asn	Leu	Leu	Asn	Tyr	Cys	Phe	Gln	Thr	Phe	Leu	Asp	Lys	Thr
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Val	Pro	Ala	Thr	Leu	Pro	Gln	Leu	Thr	Pro	Thr	Leu	Val	Ser	Leu	Leu																																							
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g	a	g	g	t	t	a	t	t	g	a	a	c	c	t	g	a	a	c	t	t	a	t	a	t	g	c	a	g	a	c	t	g	a	t	a	g	c	t	c	t	g	t	t	g		96								
Glu	Val	Ile																																																				
				20					25																																													
c	c	a	g	a	c	t	a	c	t	a	c	t	a	c	t	a	c	t	a	c	t	a	c	t	a	c	t	a	c	t	a	c	t	a	c	t	a	c	t	a	c	t	a	c	t	g		144						
Pro	Asp	Ser	Thr	Trp	Arg	Ile	Met	Thr	Thr	Leu	Asn	Met	Leu	Gly	Gly																																							
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Arg	Gln	Val	Ile	Ala	Ala	Val	Lys	Trp	Ala	Lys	Ala	Ile	Pro	Gly	Phe																																							
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Arg	Asn	Leu	His	Leu	Asp	Asp	Gln	Met	Thr	Leu	Leu	Gln	Tyr	Ser	Trp																																							
				65			70					75																																										
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Met	Ser	Leu	Met	Ala	Phe	Ala	Leu	Gly	Trp	Arg	Ser	Tyr	Arg	Gln	Ser																																							
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Ser	Ala	Asn	Leu	Leu	Cys	Phe	Ala	Pro	Asp	Leu	Ile	Ile	Asn	Glu	Gln																																							
				100				105					110																																									
a	g	a	a	c	c	t	a	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c		384				
Arg	Met	Thr	Leu	Pro	Cys	Met	Tyr	Asp	Gln	Cys	Lys	His	Met	Leu	Tyr																																							
				115			120					125																																										
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Val	Ser	Ser	Glu	Leu	His	Arg	Leu	Gln	Val	Ser	Tyr	Glu	Glu	Tyr	Leu																																							
				130			135					140																																										
t	g	t	a	t	a	a	a	c	c	t	a	a	c	c	t	a	a	c	c	t	a	a	c	c	t	a	a	c	c	t	a	a	c	c	t	a	a	c	c	t	a	a	c	c	t	a	a	c	c	t	g		480	
Cys	Met	Lys	Thr	Leu	Leu	Leu	Leu	Ser	Ser	Val	Pro	Lys	Asp	Gly	Leu																																							
				145			150					155																																										
a	a	g	a	c	a	a	c	a	a	c	a	a	c	a	a	c	a	a	c	a	a	c	a	a	c	a	a	c	a	a	c	a	a	c	a	a	c	a	a	c	a	a	c	a	a	c	a	a	c	g		528		
Lys	Ser	Gln	Glu	Leu	Phe	Asp	Glu	Ile	Arg	Met	Thr	Tyr	Ile	Lys	Glu																																							
				165								170																																										
c	t	a	g	a	a	c	a	a	c	a	a	c	a	a	c	a	a	c	a	a	c	a	a	c	a	a	c	a	a	c	a	a	c	a	a	c	a	a	c	a	a	c	a	a	c	a	a	c	g		576			
Leu	Gly	Lys	Ala	Ile	Val	Lys	Arg	Glu	Gly	Asn	Ser	Ser	Gln	Asn	Trp																																							
				180				185					190																																									
c	a	g	c	g	t	t	t	a	t	a	c	a	a	c	a	a	c	a	a	c	a	a	c	a	a	c	a	a	c	a	a	c	a	a	c	a	a	c	a	a	c	a	a	c	a	a	c	g		624				

Gln	Arg	Phe	Tyr	Gln	Leu	Thr	Lys	Leu	Leu	Asp	Ser	Met	His	Glu	Val		
		195					200					205					
gtt	gaa	aat	ctc	ctt	aac	tat	tgc	ttc	caa	aca	ttt	ttg	gat	aag	acc	672	
Val	Glu	Asn	Leu	Leu	Asn	Tyr	Cys	Phe	Gln	Thr	Phe	Leu	Asp	Lys	Thr		
	210					215					220						
atg	agt	att	gaa	ttc	ccc	gag	atg	tta	gct	gaa	atc	atc	acc	aat	cag	720	
Met	Ser	Ile	Glu	Phe		Glu	Met	Leu	Ala	Glu	Ile	Ile	Thr	Asn	Gln		
225					230					235					240		
ata	cca	aaa	tat	tca	aat	gga	aat	atc	aaa	aaa	ctt	ctg	ttt	cat	caa	768	
Ile	Pro	Lys	Tyr	Ser	Asn	Gly	Asn	Ile	Lys	Lys	Leu	Leu	Phe	His	Gln		
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Lys	*																

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 <213> Homo sapiens

<400> 8

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Arg	Asn	Leu	His	Leu	Asp	Asp	Gln	Met	Thr	Leu	Leu	Gln	Tyr	Ser	Trp		
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Ser	Ala	Asn	Leu	Leu	Cys	Phe	Ala	Pro	Asp	Leu	Ile	Ile	Asn	Glu	Gln		
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Arg	Met	Thr	Leu	Pro	Cys	Met	Tyr	Asp	Gln	Cys	Lys	His	Met	Leu	Tyr		
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Val	Ser	Ser	Glu	Leu	His	Arg	Leu	Gln	Val	Ser	Tyr	Glu	Glu	Tyr	Leu		
	130					135					140						
Cys	Met	Lys	Thr	Leu	Leu	Leu	Ser	Ser	Val	Pro	Lys	Asp	Gly	Leu			
145					150				155					160			
Lys	Ser	Gln	Glu	Leu	Phe	Asp	Glu	Ile	Arg	Met	Thr	Tyr	Ile	Lys	Glu		
				165					170					175			
Leu	Gly	Lys	Ala	Ile	Val	Lys	Arg	Glu	Gly	Asn	Ser	Ser	Gln	Asn	Trp		
			180					185					190				
Gln	Arg	Phe	Tyr	Gln	Leu	Thr	Lys	Leu	Leu	Asp	Ser	Met	His	Glu	Val		
		195					200					205					
Val	Glu	Asn	Leu	Leu	Asn	Tyr	Cys	Phe	Gln	Thr	Phe	Leu	Asp	Lys	Thr		
	210					215					220						
Met	Ser	Ile	Glu	Phe	Pro	Glu	Met	Leu	Ala	Glu	Ile	Ile	Thr	Asn	Gln		
225					230					235					240		
Ile	Pro	Lys	Tyr	Ser	Asn	Gly	Asn	Ile	Lys	Lys	Leu	Leu	Phe	His	Gln		
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Lys

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 Leu Leu Ser Thr Leu Asn Arg Leu Ala Gly Lys Gln Met Ile Gln Val
 35 40 45
 Val Lys Trp Ala Lys Val Leu Pro Gly Phe Lys Asn Leu Pro Leu Glu
 50 55 60
 Asp Gln Ile Thr Leu Ile Gln Tyr Ser Trp Met Cys Leu Ser Ser Phe
 65 70 75 80
 Ala Leu Ser Trp Arg Ser Tyr Lys His Thr Asn Ser Gln Phe Leu Tyr
 85 90 95
 Phe Ala Pro Asp Leu Val Phe Asn Glu Glu Lys Met His Gln Ser Ala
 100 105 110
 Met Tyr Glu Leu Cys Gln Gly Met His Gln Ile Ser Leu Gln Phe Val
 115 120 125
 Arg Leu Gln Leu Thr Phe Glu Glu Tyr Thr Ile Met Lys Val Leu Leu
 130 135 140
 Leu Leu Ser Thr Ile Pro Lys Asp Gly Leu Lys Ser Gln Ala Ala Phe
 145 150 155 160
 Glu Glu Met Arg Thr Asn Tyr Ile Lys Glu Leu Arg Lys Met Val Thr
 165 170 175
 Lys Cys Pro Asn Asn Ser Gly Gln Ser Trp Gln Arg Phe Tyr Gln Leu
 180 185 190
 Thr Lys Leu Leu Asp Ser Met His Asp Leu Val Ser Asp Leu Leu Glu

65					70					75				80
Ala	Met	Gly	Trp	Arg	Ser	Phe	Thr	Asn	Val	Asn	Ser	Arg	Met	Leu
				85					90					95
Phe	Ala	Pro	Asp	Leu	Val	Phe	Asn	Glu	Tyr	Arg	Met	His	Lys	Ser
			100					105					110	
Met	Tyr	Ser	Gln	Cys	Val	Arg	Met	Arg	His	Leu	Ser	Gln	Glu	Phe
		115					120					125		Gly
Trp	Leu	Gln	Ile	Thr	Pro	Gln	Glu	Phe	Leu	Cys	Met	Lys	Ala	Leu
	130					135					140			Leu
Leu	Phe	Ser	Ile	Ile	Pro	Val	Asp	Gly	Leu	Lys	Asn	Gln	Lys	Phe
145					150					155				Phe
Asp	Glu	Leu	Arg	Met	Asn	Tyr	Ile	Lys	Glu	Leu	Asp	Arg	Ile	Ile
				165					170					Ala
Cys	Lys	Arg	Lys	Asn	Pro	Thr	Ser	Cys	Ser	Arg	Arg	Phe	Tyr	Gln
			180					185					190	Leu
Thr	Lys	Leu	Leu	Asp	Ser	Val	Gln	Pro	Ile	Ala	Arg	Glu	Leu	His
	195						200					205		Gln
Phe	Thr	Phe	Asp	Leu	Leu	Ile	Lys	Ser	His	Met	Val	Ser	Val	Asp
	210					215					220			Phe
Pro	Glu	Met	Met	Ala	Glu	Ile	Ile	Ser	Val	Gln	Val	Pro	Lys	Ile
225					230					235				Leu
Ser	Gly	Lys	Val	Lys	Pro	Ile	Tyr	Phe	His	Thr	Gln			
				245					250					